

RECEIVED 11/15/91



**BAYLOR
COLLEGE OF
MEDICINE**

One Baylor Plaza
Houston, Texas 77030

Institute for
Molecular Genetics
(713) 798-4774
FAX (713) 798-7383

November 4, 1991

Victor A. McKusick, M.D.
University Professor of Medical Genetics
The Johns Hopkins Hospital
600 N. Wolfe Street
Blalock 1007
Baltimore, Maryland 21205

Dear Victor:

I am concerned about our National Research Council of the National Academy of Sciences' (NRC/NAS) report related to the quality and recommendations of the population genetics section of the report. In my opinion the report does not represent the consensus, wisdom, and science of population genetics. We have a most powerful identification system - DNA variation - which can serve the public well in the circumstances of violent crime investigation. By the choice of outlier examples of old protein polymorphisms population data, a straw man has been made which if followed to a recommended end point has trivialized the significance of matching VNTRs. The 1/N final recommendation ignores published and available DNA data sets and population genetic principles. I have attached a copy of my letter published in the *American Journal of Human Genetics* (AJHG; 49:893-895, 1991) which proposes alternative ways of estimating the significance of match. I recommend option 3 until a more accurate method is documented. I feel the range of values is more scientifically sound than 1/N (option 1). The lack of our meeting to resolve these differences of opinions was unfortunate. The process by which we arrived at the final recommendations is unacceptable to me and thus I have to oppose the final report. I am very sorry for this outcome. The courts would have profited by a consensus report. Let me make a few points which I feel should be taken into account.

- 1) Since the report deals with VNTR DNA data, I recommend published population data of VNTR type be used (Budowle *et al.*, AJHG 48:841-855, 1991; Baird *et al.*, AJHG 39:489-501, 1986.). Make points on the DNA data not old protein polymorphism data.
- 2) Do not use outlier data to make a recommendation from the NAS which ignores principles of population genetics. Rather estimate how wide a range of variation

could be expected for 1-8 band matches. Then recommend how to use population genetics principles to calculate significance of match.

- 3) The recent data of Jeffreys reported in *Cell*(60:473-485, 1990) and at the *International Congress of Human Genetics* (Abstract #2789, 49:489, 1991) is quite enlightening on how much we are underestimating DNA variation based on band size (RFLP). This feature together with fixed or variable bin methods for estimating the significance of match are needed in our report. My opinion as a molecular biologist is that current methods of calculating VNTR match significance is very conservative and greatly compensates for rare allele frequency differences between two population data sets. The majority of DNA forensic reports presented in court are based on >4 RFLPs and generally 6-8. Matches with 3-4 probes minimizes an single - rider RFLP allele frequency differences between the data sets wrongly including an individual or affecting the significance of match calculation. I illustrated this in my letter to the *AJHG* (49:893-895, 1991).
- 4) I suggest that a more reasonable way of estimating a significance of match is option 3 given in my letter. I recommend a Caucasian defendant should have his/her match significance calculated against the most appropriate data base - Caucasian. The courts should also be informed of the significance of match against the data bases of Afro Americans and Mexican Americans. Such estimated are based on genetic principles. I have no objection to our reassuring the court that a match has been searched for N individuals and either been found or not found.
- 5) The acquisition of new data from a variety of ethnic groups I find supportable. A great deal is currently available by request from International Forensic Laboratories. How the data is used to determine a ceiling value, as recommended by the NAS' report, I predict would be quite debatable among population geneticists. Unless a utility could be agreed on by leading population geneticists, prior to this expensive study, I am not enthusiastic about the expenditure of law enforcement funds. It could be a misdirected expenditure for NIJ and FBI. Unfortunately, they do

Dr. Victor McKusick
November 4, 1991
Page 3 of 3

not have limitless budgets and thus such an NAS recommendation must have accountability to U.S. tax payers when rising crime is so demanding on NIJ and FBI resources. What is the price? Does it lead to a forensic science solution? Does it simply raise more population genetic research questions.

Victor, I know you have worked harder than any of us on this report. I have great respect for your dedication and sincerity. I do not wish to see NAS made an error or more importantly for the American public's interest to be wrongly served. We have a technology at hand which can serve the public against violent criminals. The report has misrepresented the power of the DNA technology for personal identification.

Give me a call. I would love to meet with the Committee on the final report. I would give it my highest priority. We really need a consensus report.

Sincerely,

A handwritten signature in black ink, appearing to be 'C. Thomas Caskey', written over a horizontal line.

C. Thomas Caskey, M.D., F.A.C.P.
Henry and Emma Meyer Professor
Director, Institute for Molecular Genetics

CTC/emp
Enclosure